



1600

## RAW SEQUENCE LISTING

DATE: 12/12/2002

PATENT APPLICATION: US/09/332,522D

TIME: 10:17:53

Input Set : N:\Crf4\12032002\I332522.raw

Output Set: N:\CRF4\12122002\I332522D.raw

1 <110> APPLICANT: Costa, M.  
 2 Doberstein, S.  
 3 Elson, S.  
 4 Ferguson, K.  
 5 Homberger, S.  
 6 <120> TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM  
 AND SCREENING  
 7 OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METABOLISM  
 8 <130> FILE REFERENCE: 7326-101, EX99-004  
 9 <140> CURRENT APPLICATION NUMBER: US/09/332,522D  
 10 <141> CURRENT FILING DATE: 1999-06-14  
 11 <160> NUMBER OF SEQ ID NOS: 95  
 12 <170> SOFTWARE: PatentIn version 3.1  
 14 <210> SEQ ID NO: 1  
 15 <211> LENGTH: 3419  
 16 <212> TYPE: DNA  
 17 <213> ORGANISM: Caenorhabditis elegans  
 18 <400> SEQUENCE: 1

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21	cgctcgattt	tgacatggag	cacaactggc	aagagcccgg	accatcacaa	caaccggatc	180
22	catcaattcc	cggaaatcaa	cacagtccgc	cacaggaata	ttatgatatt	gatggtcaac	240
23	gagacgtaag	caccttacac	tccctgctca	accacaacaa	cgacgacttc	ttctcaatgc	300
24	gattttcccc	gccaaacttt	gatctcggcg	gaggccgtgg	accttctcta	gccgccaccc	360
25	aacaattatc	tggagaaggt	cctgcaagta	tgcttaaccc	cttacaacaa	tctccaccaa	420
26	gtggagggtta	ccccccggca	gatgcctaca	gacctctatc	acttgctcaa	caactcgccg	480
27	cgccagcgat	gactccacat	caggcagcgt	cgctttttgt	taataactaat	ggaattgatc	540
28	aaaagaattt	cactcatgca	atgctatctt	caccacacca	tacctcaatg	acttctcaac	600
29	catatacaga	agccatggga	catatcaacg	ggtacatgtc	tccatacgac	caagctcaag	660
30	gcccatcagg	accatcatat	tactcacaac	accatcaatc	tccaccacct	catcaccacc	720
31	atcaccaccc	gatgccaaaa	atccatgaga	accctgaaca	agtggcatct	ccatcgattg	780
32	aagatgctcc	agagacgaaa	ccaactcatt	tggttgaacc	acaaagtcca	aaaagcccgc	840
33	agaatatgaa	agaggagctt	cttcgggttac	tagttaacat	gtctccgagt	gaagttgaac	900
34	ggttaaagaa	taaaaaatca	ggagcatggt	cagcgacgaa	tgggccatcg	aggagtaagg	960
35	agaaggcggc	gaagattgtg	attcaggaga	cagcgggaag	ggatgaagat	gaggatgatg	1020
36	aggatagtga	ttccggggag	actatgtctc	agggaactac	tattattggt	cgaagaccaa	1080
37	aaaccgagcg	tcgtacggca	cacaatctca	tcgaaaagaa	gtatagatgc	tcaataaatg	1140
38	atcgaattca	acagctgaaa	gtacttttgt	gtggggatga	agctaagctt	tcaaaatcgg	1200
39	caacactacg	acgggctatt	gaacatatcg	aggagggtga	acacgagaat	cagggtgttg	1260
40	agcatcatgt	tgaacaaatg	agaaagacac	tgcagaataa	tcgattaccg	tacccggaac	1320
41	caattcaata	cactgaatac	tctgcccgat	caccgcgcga	atcatctcct	tctccacctt	1380
42	gaaatgagag	aaaacgatca	cgaatgagca	caacgactcc	tatgaagaat	ggaactagag	1440
43	atggatcttc	gaaagttacc	ctttttgcga	tgctcctagc	agttctgatt	tttaatccga	1500
44	ttggattgct	cgctggaagt	gcgatattct	caaaagccgc	tgcagaagct	ccgattgcct	1560

Does Not Comply  
 Corrected Diskette Reader

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45      ccccggttcga gcatggaaga gtgattgatg acccggatgg aactagcact cggacgcttt 1620
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47      tatatgtggt tgtcaaaactg ctgatccatg gtgaccctgt tcaagacttc atgtccgttt 1740
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62      ttgatgtttc aagacttttg gtgacaattt caacgcagtg cgctgccatt ttgactaatg 2640
63      agaaggatga gtcagcgaaa ttcggaacct ggatctctcg aaacggagat gcttgttgca 2700
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71      aggcgtataa tcattatgcg attattaatg ggacaagggg agattgttg agactatttg 3180
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74      cggctcaacc ggacgcattt catcttcata cactggttaa actacatact tctatggatc 3360
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77 &lt;210&gt; SEQ ID NO: 2

78 &lt;211&gt; LENGTH: 1113

79 &lt;212&gt; TYPE: PRT

80 &lt;213&gt; ORGANISM: Caenorhabditis elegans

81 &lt;220&gt; FEATURE:

82 &lt;221&gt; NAME/KEY: misc feature

83 &lt;222&gt; LOCATION: (1073)..(1073)

84 &lt;223&gt; OTHER INFORMATION: "X" is any amino acid

85 &lt;400&gt; SEQUENCE: 2

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87      1              5              10              15
88      Ser Leu Val Thr Lys Leu Asp Asp Ile Ala Pro Phe Pro Asn Asn Asp
89      20              25              30
90      Pro Leu Asp Phe Asp Met Glu His Asn Trp Gln Glu Pro Gly Pro Ser
91      35              40              45
92      Gln Gln Pro Asp Pro Ser Ile Pro Gly Asn Gln His Ser Pro Pro Gln
93      50              55              60
94      Glu Tyr Tyr Asp Ile Asp Gly Gln Arg Asp Val Ser Thr Leu His Ser

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95	65	70	75	80
96	Leu Leu Asn His Asn Asn Asp Asp Phe Phe Ser Met Arg Phe Ser Pro			
97	85	90	95	
98	Pro Asn Phe Asp Leu Gly Gly Gly Arg Gly Pro Ser Leu Ala Ala Thr			
99	100	105	110	
100	Gln Gln Leu Ser Gly Glu Gly Pro Ala Ser Met Leu Asn Pro Leu Gln			
101	115	120	125	
102	Thr Ser Pro Pro Ser Gly Gly Tyr Pro Pro Ala Asp Ala Tyr Arg Pro			
103	130	135	140	
104	Leu Ser Leu Ala Gln Gln Leu Ala Ala Pro Ala Met Thr Pro His Gln			
105	145	150	155	160
106	Ala Ala Ser Leu Phe Val Asn Thr Asn Gly Ile Asp Gln Lys Asn Phe			
107	165	170	175	
108	Thr His Ala Met Leu Ser Ser Pro His His Thr Ser Met Thr Ser Gln			
109	180	185	190	
110	Pro Tyr Thr Glu Ala Met Gly His Ile Asn Gly Tyr Met Ser Pro Tyr			
111	195	200	205	
112	Asp Gln Ala Gln Gly Pro Ser Gly Pro Ser Tyr Tyr Ser Gln His His			
113	210	215	220	
114	Gln Ser Pro Pro Pro His His His His His Pro Met Pro Lys Ile			
115	225	230	235	240
116	His Glu Asn Pro Glu Gln Val Ala Ser Pro Ser Ile Glu Asp Ala Pro			
117	245	250	255	
118	Glu Thr Lys Pro Thr His Leu Val Glu Pro Gln Ser Pro Lys Ser Pro			
119	260	265	270	
120	Gln Asn Met Lys Glu Glu Leu Leu Arg Leu Leu Val Asn Met Ser Pro			
121	275	280	285	
122	Ser Glu Val Glu Arg Leu Lys Asn Lys Lys Ser Gly Ala Cys Ser Ala			
123	290	295	300	
124	Thr Asn Gly Pro Ser Arg Ser Lys Glu Lys Ala Ala Lys Ile Val Ile			
125	305	310	315	320
126	Gln Glu Thr Ala Glu Gly Asp Glu Asp Glu Asp Asp Glu Asp Ser Asp			
127	325	330	335	
128	Ser Gly Glu Thr Met Ser Gln Gly Thr Thr Ile Ile Val Arg Arg Pro			
129	340	345	350	
130	Lys Thr Glu Arg Arg Thr Ala His Asn Leu Ile Glu Lys Lys Tyr Arg			
131	355	360	365	
132	Cys Ser Ile Asn Asp Arg Ile Gln Gln Leu Lys Val Leu Leu Cys Gly			
133	370	375	380	
134	Asp Glu Ala Lys Leu Ser Lys Ser Ala Thr Leu Arg Arg Ala Ile Glu			
135	385	390	395	400
136	His Ile Glu Glu Val Glu His Glu Asn Gln Val Leu Lys His His Val			
137	405	410	415	
138	Glu Gln Met Arg Lys Thr Leu Gln Asn Asn Arg Leu Pro Tyr Pro Glu			
139	420	425	430	
140	Pro Ile Gln Tyr Thr Glu Tyr Ser Ala Arg Ser Pro Val Glu Ser Ser			
141	435	440	445	
142	Pro Ser Pro Pro Arg Asn Glu Arg Lys Arg Ser Arg Met Ser Thr Thr			
143	450	455	460	

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Output Set: N:\CRF4\12122002\I332522D.raw

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144 Thr Pro Met Lys Asn Gly Thr Arg Asp Gly Ser Ser Lys Val Thr Leu
145 465 470 475 480
146 Phe Ala Met Leu Leu Ala Val Leu Ile Phe Asn Pro Ile Gly Leu Leu
147 485 490 495
148 Ala Gly Ser Ala Ile Phe Ser Lys Ala Ala Ala Glu Ala Pro Ile Ala
149 500 505 510
150 Ser Pro Phe Glu His Gly Arg Val Ile Asp Asp Pro Asp Gly Thr Ser
151 515 520 525
152 Thr Arg Thr Leu Phe Trp Glu Gly Ser Ile Ile Asn Met Ser Tyr Val
153 530 535 540
154 Trp Val Phe Asn Ile Leu Met Ile Ile Tyr Val Val Val Lys Leu Leu
155 545 550 555 560
156 Ile His Gly Asp Pro Val Gln Asp Phe Met Ser Val Ser Trp Gln Thr
157 565 570 575
158 Phe Val Thr Thr Arg Glu Lys Ala Arg Ala Glu Leu Asn Ser Gly Asn
159 580 585 590
160 Leu Lys Asp Ala Gln Arg Lys Phe Cys Glu Cys Leu Ala Thr Leu Asp
161 595 600 605
162 Arg Ser Leu Pro Ser Pro Gly Val Asp Ser Val Phe Ser Val Gly Trp
163 610 615 620
164 Glu Cys Val Arg His Leu Leu Asn Trp Leu Trp Ile Gly Arg Tyr Ile
165 625 630 635 640
166 Ala Arg Arg Arg Arg Ser Thr Thr Lys Pro Val Ser Val Val Cys Arg
167 645 650 655
168 Ser His Ala Gln Thr Ala Val Leu Tyr His Glu Ile His Gln Leu His
169 660 665 670
170 Leu Met Gly Ile Thr Gly Asn Phe Glu Asp Thr Tyr Glu Pro Ser Ala
171 675 680 685
172 Leu Thr Gly Leu Phe Met Ser Leu Cys Ala Val Asn Leu Ala Glu Ala
173 690 695 700
174 Ala Gly Ala Ser Asn Asp Gly Leu Pro Arg Ala Val Met Ala Gln Ile
175 705 710 715 720
176 Tyr Ile Ser Ala Ser Ile Gln Cys Arg Leu Ala Leu Pro Asn Leu Leu
177 725 730 735
178 Ala Pro Phe Phe Ser Gly Tyr Phe Leu Arg Arg Ala Arg Arg His Val
179 740 745 750
180 Arg Arg Ala Pro Glu His Ser Val Ser His Leu Leu Trp Ile Phe His
181 755 760 765
182 Pro Ala Thr Arg Lys Phe Met Ser Asp Ala Lys Arg Leu Glu His Val
183 770 775 780
184 Leu Ser Ser Lys Gln Lys Gln Leu Arg Phe Gly Ser Phe Val Glu Asp
185 785 790 795 800
186 Glu Gln Leu Ser Pro Leu Ala Arg Ile Arg Thr Thr Leu Lys Val Tyr
187 805 810 815
188 Leu Leu Ser Lys Leu Val Gln Glu Leu Val Gly Gly Asp Glu Ile Phe
189 820 825 830
190 Thr Lys Asn Val Glu Arg Ile Leu Asn Asp Asn Asp Arg Leu Asp Asp
191 835 840 845
192 Glu Val Asp Val Val Asp Val Ser Arg Leu Leu Val Thr Ile Ser Thr

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197      885      890      895
198      His Val Leu Thr Cys Gly Ile Tyr Trp Arg Ser Asn Lys Asn Glu Leu
199      900      905      910
200      Ala Arg Gln His Tyr Ser Leu Ile Arg Asn Cys Pro Pro Lys Ile Leu
201      915      920      925
202      Thr Asp Asn Leu Gly Leu Ala Val Gly His Ala Leu Cys Ala Arg Lys
203      930      935      940
204      Ile Cys Ile Asp Asp Arg Asp Ser Pro Lys Val Ser Gln Tyr Val Cys
205      945      950      955      960
206      Ile His Thr Lys Lys Ser Leu Glu Ser Leu Arg Leu Phe Ser Thr Ser
207      965      970      975
208      Ser Arg Ala Ser Gly Val Val Ser Gly Ile Gln Glu Gly Thr Arg Arg
209      980      985      990
210      Met Ala Tyr Glu Trp Ile Met Asn Ser Leu Leu Asp Ala Trp Arg Ser
211      995      1000      1005
212      Asn Leu Phe Ala Ser Lys Pro Tyr Trp Thr Gln Ser Phe Lys Gly
213      1010      1015      1020
214      Gln Ser Thr Phe Ser Thr Leu Tyr Gln Glu Ala Tyr Asn His Tyr
215      1025      1030      1035
216      Ala Ile Ile Asn Gly Thr Arg Gly Asp Cys Trp Arg Leu Phe Val
217      1040      1045      1050
218      Tyr Glu Leu Thr Cys Arg Met Leu Asn Gly Ala Asn Pro Gln Ala
219      1055      1060      1065
W--> 220      Thr Trp Ser Gly Xaa Arg Arg Val Arg Ser Thr Lys Met Asp Ala
221      1070      1075      1080
222      Val Arg Gly Arg Val Ser Met Arg Arg Ser Ala Gln Pro Asp Ala
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234      cgcaagtgcac gtccagcaac cggaggaccc ccaactgtag aatccgcac accatccctaa      180
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237      tgcactaccc gtacgatgcc ttctcacaaga acaccgggct gagtataaat ttcattgagcc      360
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<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: :  
<400> SEQUENCE: 10  
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25

*see p. 7  
for error explanation*

The errors shown exist throughout  
the sequence. Please check subsequent  
sequences for similar errors.